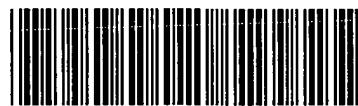


043D

OHD0



OIPE

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/10/043,787

DATE: 02/11/2002  
TIME: 10:01:45

Input Set : F:\46699-20002.txt  
Output Set: N:\CRF3\02112002\J043787.raw

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4 <110> APPLICANT: Yuan, Chong-Sheng  
 6 <120> TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR ASSAYING  
 7 HOMOCYSTEINE  
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 35 Trp Gly Arg Lys Ala Leu Asp Ile Ala Glu Asn Glu Met Pro Gly Leu  
 36 20 25 30  
 37 Met Arg Met Arg Glu Arg Tyr Ser Ala Ser Lys Pro Leu Lys Gly Ala  
 38 35 40 45  
 39 Arg Ile Ala Gly Cys Leu His Met Thr Val Glu Thr Ala Val Leu Ile  
 40 50 55 60  
 41 Glu Thr Leu Val Thr Leu Gly Ala Glu Val Gln Trp Ser Ser Cys Asn  
 42 65 70 75 80  
 43 Ile Phe Ser Thr Gln Asn His Ala Ala Ala Ile Ala Lys Ala Gly  
 44 85 90 95  
 45 Ile Pro Val Tyr Ala Trp Lys Gly Glu Thr Asp Glu Glu Tyr Leu Trp  
 46 100 105 110  
 47 Cys Ile Glu Gln Thr Leu Tyr Phe Lys Asp Gly Pro Leu Asn Met Ile  
 48 115 120 125  
 49 Leu Asp Asp Gly Gly Asp Leu Thr Asn Leu Ile His Thr Lys Tyr Pro  
 50 130 135 140  
 51 Gln Leu Leu Pro Gly Ile Arg Gly Ile Ser Glu Glu Thr Thr Gly  
 52 145 150 155 160  
 53 Val His Asn Leu Tyr Lys Met Met Ala Asn Gly Ile Leu Lys Val Pro  
 54 165 170 175  
 55 Ala Ile Asn Val Asn Asp Ser Val Thr Lys Ser Lys Phe Asp Asn Leu  
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57 Tyr Gly Cys Arg Glu Ser Leu Ile Asp Gly Ile Lys Arg Ala Thr Asp  
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 59 Val Met Ile Ala Gly Lys Val Ala Val Val Ala Gly Tyr Gly Asp Val  
 60 210 215 220  
 61 Gly Lys Gly Cys Ala Gln Ala Leu Arg Gly Phe Gly Ala Arg Val Ile  
 62 225 230 235 240  
 63 Ile Thr Glu Ile Asp Pro Ile Asn Ala Leu Gln Ala Ala Met Glu Gly  
 64 245 250 255  
 65 Tyr Glu Val Thr Thr Met Asp Glu Ala Cys Gln Glu Gly Asn Ile Phe  
 66 260 265 270  
 67 Val Thr Thr Gly Cys Ile Asp Ile Ile Leu Gly Arg His Phe Glu  
 68 275 280 285  
 69 Gln Met Lys Asp Asp Ala Ile Val Cys Asn Ile Gly His Phe Asp Val  
 70 290 295 300  
 71 Glu Ile Asp Val Lys Trp Leu Asn Glu Asn Ala Val Glu Lys Val Asn  
 72 305 310 315 320  
 73 Ile Lys Pro Gln Val Asp Arg Tyr Arg Leu Lys Asn Gly Arg Arg Ile  
 74 325 330 335  
 75 Ile Leu Leu Ala Glu Gly Arg Leu Val Asn Leu Gly Cys Ala Met Gly  
 76 340 345 350  
 77 His Pro Ser Phe Val Met Ser Asn Ser Phe Thr Asn Gln Val Met Ala  
 78 355 360 365  
 79 Gln Ile Glu Leu Trp Thr His Pro Asp Lys Tyr Pro Val Gly Val His  
 80 370 375 380  
 81 Phe Leu Pro Lys Lys Leu Asp Glu Ala Val Ala Glu Ala His Leu Gly  
 82 385 390 395 400  
 83 Lys Leu Asn Val Lys Leu Thr Lys Leu Thr Glu Lys Gln Ala Gln Tyr  
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 96 ctgagaacga gatgccgggc ctgatgcgtt tgcgggagcg gtactcgccc tccaaaggcc 180  
 97 tgaaggcgcc ccgcatcgct ggctgcctgc acatgaccgt ggagacggcc gtcctcattg 240  
 98 agaccctcgta caccctgggt gctgaggtgc agtggtccag ctgcaacatc ttctccaccc 300  
 99 agaaccatgc ggcggctgcc attgccaagg ctggcattcc ggtgtatgcc tggaaggcg 360  
 100 aaacggacga ggagttacctg tggtgcatcg agcagaccct gtacttcaag gacggggccc 420  
 101 tcaacatgtat tctggacgac gggggcgacc tcaccaacct catccacacc aagtacccgc 480  
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 104 ccaagagcaa gtttgacaac ctctatggct gccgggagtc cctcatagat ggcattcaagc 660  
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110	tctgtccctg	acaatctccc	acggtcttgg	gctgcctgac	aggcactttg	agcagatgaa	1020
111	ggatgtgcc	attgtgtgta	acattggaca	cttgcgtgt	gagatcgatg	tcaagtggct	1080
112	caacgagaac	gccgtggaga	aggtaacat	caagccgcag	gtggaccgg	atcggttgaa	1140
113	aatgggcgc	cgcacatcc	tgctggccga	gggtcggt	gtcaacctgg	gttgtgccc	1200
114	ggccacccc	agcttcgtga	tgagtaactc	cttcaccaac	cagggtatgg	cgcagatcga	1260
115	gctgtggacc	catccagaca	agtacccgt	tgggttcat	ttcctgccc	agaagctgga	1320
116	tgaggcagtg	gctgaagccc	acctggcaa	gctgaatgt	aaggtagcca	agctaactga	1380
117	gaagcaagcc	cagtacctgg	gcatgtcctg	tgatggcccc	ttcaagccgg	atactaccg	1440
118	ctactgagag	ccaggctctgc	gtttcacct	ccagctgt	tccttggcc	ggcccccacct	1500
119	ctcctcccta	agagctaatt	gcaccaactt	tgtgattgt	ttgtcagtgt	ccccccatcga	1560
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121	gtggcagogg	gaacagagta	cccttctcaa	gccccgtca	tgatggaggt	cccagccaca	1680
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123	aagtcaatg	tggagtca	aagccatgt	gttttgcatt	ctaggcccttc	acctggcttg	1800
124	tggacttata	cctgtgtgct	tggtttacag	gtccagtggt	tcttcagccc	atgacagatg	1860
125	agaaggggct	atattgaagg	gcaaagagga	actgttgg	gaattttct	gagagcctgg	1920
126	cttagtgctg	ggccttctct	taaacctcat	tacaatgagg	ttagtactt	tagtccctgt	1980
127	tttacagggg	ttagaataga	ctgttaaggg	gcaactgaga	aagaacagag	aagtgacagc	2040
128	taggggttga	gagggccag	aaaaacatga	atgcaggcag	attcgtgaa	atctgccacc	2100
129	actttataac	cagatggttc	cttcacaaac	cctggtcaa	aaagagaata	atttggccta	2160
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144	gcaaaatatac	tgggactcaa	aaaaatggg	ccattcaac	ctaatttatta	cagatactaa	120
145	tggaccatac	taccaaggac	cagtccacct	gaaccacaca	ctctaaagaa	atatttttta	180
146	agataacttt	tatttcttc	ttactcctt	cctcttgatt	tttttccat	aatttcattc	240
147	ttgttttttc	atctcattat	ccaaatgt	cagaccacac	aggaacttgc	ttcatggctc	300
148	tttagatgaa	atagaagttc	agggtccctc	actctagtca	ctaaagaagg	attttactct	360
149	cccagccca	aaagggtatt	ctttctttac	catttctggg	gactttagtc	ttaatttaggt	420
150	actttattaa	cagaaaatgc	taaggtacct	tctctgtgga	acaatctgca	atgtctaaat	480
151	cgccttaaaa	gagccattt	cttagctgt	gaaatcgt	ctctttca	tcttcagaga	540
152	agcagggatg	gtacctaccc	ggcaggtagg	ttagatgtgg	gtggtgcatg	ttaatttccc	600
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161	tactcagtat aaagcactga gttctatctt taggatttat cttaagagc aaatttctgg	1140
162	ttagttatgc ttctgcaacc taaaatattt aaaggagggt aggtgtggc aggaggagga	1200
163	atgataaatt gggccagggc aagaaaaatc tagttcata taatttgctc gggactatac	1260
164	accctatata atgttagtt tacagaagta atatgacttt tgattgtcac ataccacaaa	1320
165	gagtttatga actgagatca taaagggcaa ctgatgtgtg aagaaagtag tcagttacatc	1380
166	ctggctcatg ctctgaaaga atatccagag aggctcttc aaagatcagg gagatgtatt	1440
167	cccatgccat gcaccctgct tcccaggatt tctgcatggt caagttagt ttatgctcat	1500
168	gagcttaag tatataatta tccaggattt taaatcctca acttggctta gcttggatc	1560
169	cctcaaagggt gggtcatacg ttatgtctatc atactagaaa ttttcacttt tccactgtatc	1620
170	agagagacag acattaaaaaa caaaaataga agaaaggaaa gcttcaccc tgcaatgttct	1680
171	tagcagggaa caattgtctt gccaaaacctt ttttccctt tctctccat tttcttttac	1740
172	ccaatccctt cttaatcctt gccagtgtga ccattgtttc ttctctgtatc atgttaacag	1800
173	ttaaggccta tttcctcg gcaatttacc aaccaatcag aacaccat ctgttaggg	1860
174	aggttaacctg gccaacatgt tatccatcac gttagccctg ctggaggggaa gggaccacaca	1920
175	ttcacctgcc ctctgacctg ccccttgcattt ccattatctat taccgtgtcc ataggaataa	1980
176	taggttaaggg ctctgtctct gtcaaggcat gtaacaaagg acactgtttaa aaaaaaaaaaa	2040
177	aagtctggca tcagagggag catgtggaga gcaacttggg aagaacaagt tcattttgtatc	2100
178	ttgaatgtattttaatgaat gcaatattaa tccttgcaga tgagcaataa tcattttatc	2160
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226 <400> SEQUENCE: 7  
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232 <213> ORGANISM: Artificial Sequence  
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270 <220> FEATURE:  
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277 <210> SEQ ID NO: 12  
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282 <220> FEATURE:  
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VERIFICATION SUMMARY  
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L:179 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3  
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